



Db	96 tppappedgrgpgagnasrdgrpsgggrpprpskappkerkw 140 : : :: :   :   :   :   :   :   :   :   :   : Qy 274 SPARPAEATSLLEGALSGTRSHPSYGRQHAGGPPSTSRRP-PRPW 317	RESULT 3 ID R50238 standard; Protein: 402 AA. AC R50238; DT 11-OCT-1994 (first entry) DE Human OP-2; KW OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDP-1(fx); 60A(fx); Bap3(fx); Bap5(fx); BMP6 (fx); osteogenic protein; morphogen; morphogenic protein; DE Full length sequence of human osteogenic protein 2 (hop-2). KW liver; regeneration; injury; cancer; integration; KW embryogenesis; organ maintenance; tissue-specific morphogenesis; KW arthritis; emphysema; osteoporosis; cirrhosis. OS Homo sapiens. OS Homo sapiens. PN WO940649-A. PD 31-MAR-1994.
RESULT 2 ID W36855; W36855; AC W36855; DT 10-MAR-1998 (first entry) DE Full length sequence of human osteogenic protein 2 (hop-2). KW Human osteogenic protein; OP-2; morphogen; morphogenic protein; KW embryogenesis; organ maintenance; tissue-specific morphogenesis; KW arthritis; emphysema; osteoporosis; cirrhosis. OS Homo sapiens.	Key F3 Region F4 FT protein F5 FT Region F6 FT PN US565276-A. FT PD 22-JUL-1997. FT PR 20-JUL-1994; 278729. FT PR 28-AUG-1992; US-938021. FT PR 30-AUG-1991; US-752764. FT PR 30-AUG-1991; US-752861. FT PA (CREA-) CREATIVE BIOMOLECULES INC. FT PI Cohen CM, Kuberansampath T, Oppermann H, Ozkaynak E; FT PI Pang RH, Rueger DC, Smart JE; FT DR 97-384665/35. FT Screening for compounds which modulate morphogen expression - by PT incubating in the presence of epithelial cells which contain a PT cellular gene for morphogenic protein expression PS Disclosure: Columns 61-64; 49pp; English. PS DR N-PSDB; T97881. CC The present sequence represents a human osteogenic protein-2 (hop-2). CC OP-2 proteins are a group of morphogenically active proteins. Morphogens CC are inactive when reduced, but are active as oxidised homodimers and when CC oxidised with other morphogens (e.g. W3683-62). Comparison of the amino CC acid sequences of these morphogens has identified a consensus of 6-7 CC cysteine motif at the C-terminal. Morphogenic proteins such as OP-2 play CC an important role, not only in embryogenesis, but also in tissue and CC organ maintenance and repair in mammals. They induce a developmental CC cascade of tissue-specific morphogenesis in a mammal. A novel method is CC described for screening a candidate compound for the ability to modulate CC expression of a cellular gene encoding a naturally occurring morphogenic CC protein. The candidate compound is incubated with epithelial cells which CC express the cellular gene, and after a period of time the epithelial CC cells are assayed for the presence of or the amount of the protein CC expressed by the cellular gene. A change in the level of the CC morphogenic protein relative to the level in the epithelial cells in the CC absence of the candidate compound is indicative of the ability of the CC compound to modulate expression of the cellular gene. The method can be CC used to identify compounds which can increase or decrease morphogen CC production or levels. Such compounds can be used in the treatment of, CC e.g. arthritis, emphysema, osteoporosis, kidney disease, lung diseases, CC cardiomopathy, and cirrhosis of the liver. CC Sequence 402 AA;	Query Match 1.5%; Score 125; DB 10; Length 402; Best Local Similarity 39.7%; Pred. No. 1.45e+00; Matches 25; Conservative 21; Mismatches 21; Indels 5; Gaps 5; AC R54937; DT 15-OCT-1994 (first entry) DE Osteogenic protein hop-2-PP. KW Morphogenic protein; hop-2-PP; OP-2; hop2; hop-2; OS Homo sapiens. PN WO9410203-A. PD 11-MAY-1994.
RESULT 4 ID R54937 standard; Protein: 402 AA. AC R54937; DT 02-NOV-1993; U10520. PR 03-NOV-1993; US-971091. PR 04-MAR-1993; US-029335. PR 31-MAR-1993; US-040510. PA (CREA-) CREATIVE BIOMOLECULES INC. PI Cohen CM, Kuberansampath T, Oppermann H, Ozkaynak E; PI Pang RH, Rueger DC; DR WO9410203-A. DR P-PSDB; Q65393 PT A morphogenically active protein MOP-3 - for inducing tissue	Query Match 1.5%; Score 125; DB 26; Length 402; Best Local Similarity 39.7%; Pred. No. 1.45e+00; Matches 25; Conservative 21; Mismatches 21; Indels 5; Gaps 5; AC R54937; DT 02-NOV-1993; U10520. PR 03-NOV-1993; US-971091. PR 04-MAR-1993; US-029335. PR 31-MAR-1993; US-040510. PA (CREA-) CREATIVE BIOMOLECULES INC. PI Cohen CM, Kuberansampath T, Oppermann H, Ozkaynak E; PI Pang RH, Rueger DC; DR WO9410203-A. DR P-PSDB; Q65393 PT A morphogenically active protein MOP-3 - for inducing tissue	
Db 12 glalcalcaaggppglrppp-gc-pqrllg-arerrdvgrelavlgipgr-prprappaas 67 Qy 172 GPPQLQGAAQA-RPPHASGPRRLGCERAWNHSVREAGYPLGLPAPGARRGGSASR 230	Query Match 1.5%; Score 125; DB 10; Length 402; Best Local Similarity 39.7%; Pred. No. 1.45e+00; Matches 25; Conservative 21; Mismatches 21; Indels 5; Gaps 5; AC R54937; DT 15-OCT-1994 (first entry) DE Osteogenic protein hop-2-PP. KW Morphogenic protein; hop-2-PP; OP-2; hop2; hop-2; OS Homo sapiens. PN WO9410203-A.	
Db 68 rlp 70 Qy 231 SLP 233	Query Match 1.5%; Score 125; DB 10; Length 402; Best Local Similarity 39.7%; Pred. No. 1.45e+00; Matches 25; Conservative 21; Mismatches 21; Indels 5; Gaps 5; AC R54937; DT 15-OCT-1994 (first entry) DE Osteogenic protein hop-2-PP. KW Morphogenic protein; hop-2-PP; OP-2; hop2; hop-2; OS Homo sapiens. PN WO9410203-A.	

**PT** morphogenesis in mammals  
**PS** Disclosure; Page 120-131: 164PP; English.  
**CC** A novel mouse morphogenic protein, OP3, has the sequence given in  
**CC** R5494, and is encoded by cDNA of sequence Q65390. cDNA and protein  
**CC** sequences were also provided for human osteogenic protein OP1  
**CC** (Q65391, R54935), mouse OP1 (Q65390, R34936), human OP2 (R65393,  
**CC** R54937) and mouse OP2 (Q65394, R54938) as well as the genomic DNA  
**CC** sequence of human OP2 (Q65395). Generic sequences given in R54939-  
**CC** 40 accomodate homologies between OP1, OP2, OP3 and other morphogen  
**CC** protein family members.  
**SQ** Sequence 402 AA;

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Best_Local_Similarity 39.7%; Matches 25; Conservative 12; Mismatches -21; Indels 5
Pred. No. 1.45e-00; Indels 5

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RESULT 6  
ID R57973 standard; Protein: 402 AA.  
R57973;  
DT 11-OCT-1994 (first entry)

DE	Human OP-2; OP-1; OP-2; CBMP2; Vgr(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx); tooth socket; alveolus; osteogenic protein; morphogen; morphogenic protein; periodontal tissue; regeneration; tooth implant; integration; inhibition.
KW	Homo sapiens.
PN	W09406399-A.
PD	31-MAR-1994.
PF	15-SEP-1993; US874215.
PR	15-SEP-1992; US945285.

PR 34-1229, US 222225.  
PR 31-MAR-1993; US 04-0510.  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
PI Cohen CM, Kuberanapath T, Oppermann H, Ozkaynak E;  
PI Pang RHL, Rueger DC, Smart JE;  
DR WPI; 94-11810/7/14.

PR Morphogen-induced periodontal tissue regeneration - used for integrating as implanted tooth in tooth socket or to inhibit tissue loss associated with periodontal disease or injury.  
 PT Claim 28-29; 132pp; English.  
 PS Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vg(fx), Vgr(fx), BMP1(fx) and at least 80% homology with BMP3(fx), BMP5(fx) and BMP6(fx) are useful for integrating an implant tooth in a tooth socket and for inhibiting tissue loss with periodontal disease or injury.  
 CC Sequence 402 AA.

Query Match 1.5%; Score 125; DB 9; Length 4  
 Best Local Similarity 39.7%; Pred. No. 1.45e+00;  
 Matches 25; Conservative 12; Mismatches 21; Indel

Db 68 rlp 70  
QY 231 SLP 233

**RESULT** 7  
**ID** R27291 standard; **Protein**: 402 AA.

AC K2/491;  
DT 26-FB-1993 (first entry)  
DE Human Osteogenic Protein HOP-2.  
KW Morbogen; Morbogen protein.

OS Homo sapiens.  
PN WO92153-A.  
PD 17-SEP-1992.  
PP 11-JUN-1992.  
M01000

PR 11-MAR-1991; US-6672274.  
PA (CREDIT - CREATIVE MOLECULES INC.  
PI Cohen CM, Kuberanpath T, Oppermann H, Pang RHL, Rueger

N-PSDB: DR Q28737. Compounds for increasing progenitor cell population - co-morphogen to induce proliferation, useful for inhibition

PT neoplastic growth, inducing tissue repair and in drug tissue dysfunction

PS Disclosure: Page 93-95; 132pp; English.

CC Mature hop2 is one of the preferred known morphogens which CC used in the manufacture of pharmaceuticals for inducing CC chondrogenic mammalian tissue growth, progenitor cell p CC and hepatic tissue growth and for maintaining the phenotypic CC expression of differentiated cells in a mammal. Morphogenetic CC compositions of the invention can also be used to treat CC disorders and impaired or lost immune function. Morphogenetic CC at least 70% homology with hop2 are included.

SQ Sequences 402 AA:

Query Match Similarity 1.5%; Score 125; DB 5; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 5; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 22; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalggggpgrlrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATOA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 22; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 22; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 9; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

Query Match Similarity 1.5%; Score 125; DB 9; Length 402;  
 Best Local Matches 25; Pred. No. 1.45e+00; Mismatches 12; Indels 5; Gaps 5;

Db 12 glalcalgggggrrppp-gc-pqrllg-arerrdvrellavlgipgr-prprappaas 67  
 | :| |::|:|||:|:|||:|:|||:|:|||:  
 Qy 172 GPPLYOLGAATQA-RPPHASGPRRLGGERAWNHSYREAGYPLGLPAPGARRGGSASR 230  
 Db 68 rlp 70  
 Qy 231 SLP 233

RESULT 9  
 ID W16366 standard; Protein; 402 AA.  
 AC W16366;  
 DT 26-Aug-1997 (first entry)  
 DE Human hippocampal osteogenic protein 2.  
 KW mature; osteogenic protein; hippocampus; soluble; ligand; antibody;  
 KW non-covalent; dimeric; bone morphogenetic protein; purity;  
 KW therapeutic.  
 Homo sapiens.  
 PN US5610021A.  
 PD 11-MAR-1997.

RESULT 10  
 ID R44759 standard; Protein; 402 AA.  
 AC R44759;  
 DT 06-JUN-1994 (first entry)  
 DE Human osteogenic protein Op2.  
 KW repair; vascularisation; bone; cartilage; matrix; osteoarthritis;  
 Homo sapiens.  
 OS US5266683-A.  
 PN 30-NOV-1993.  
 PR 08-APR-1988; 179406.  
 PR 08-APR-1988; US-179406.  
 PR 15-AUG-1988; US-332630.  
 PR 23-FEB-1989; US-315342.  
 PR 17-OCT-1989; US-422613.  
 PR 22-FEB-1990; US-483913.  
 PR 20-AUG-1990; US-569920.  
 PR 07-SEP-1990; US-579865.  
 PR 18-OCT-1990; US-599543.  
 PR 18-OCT-1990; US-600024.  
 PR 04-DEC-1990; US-621849.  
 PR 04-DEC-1990; US-621988.  
 PR 22-FEB-1991; US-660162.  
 PR 20-DEC-1991; US-810560.  
 PR 28-JAN-1992; US-827052.  
 PR 21-FEB-1992; US-841646.  
 PI Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL;  
 PI Rueger DC;  
 PI Rueger DC;  
 DR WPI; 93-395405/49.  
 DR N-PADB: Q53155.  
 PT New pure mammalian osteogenic proteins - induce cartilage and

PT endochondral bone formation when in association with a matrix  
 PS Claim 26; Columns 143-148; 128pp; English.  
 CC The osteogenic protein when in association with a matrix can induce  
 CC at the locus of an implant the full development cascade of  
 CC endochondral bone formation including vascularisation,  
 CC mineralisation and bone marrow differentiation. The osteogenic  
 CC protein can also be used to repair both bone and cartilage in the  
 CC treatment of osteoarthritis. This is the pre-pro form of the  
 CC protein.

SQ Sequence 402 AA;

Query Match 1.5%; Score 125; DB 8; Length 402;  
 Best Local Similarity 39.7%; Pred. No. 1.45e+00;

Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;

Db 12 glalcalggggpqrppp-gc-pqrllg-arerrdvgrellavlgpgr-prprappaas 67

Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASR 230

Db 68 rlp 70

231 SLP 233

RESULT 11 ID R33410 standard; Protein: 402 AA.

AC R33410;

DT 15-JUL-1993 (first entry)

DE Human OP-2-PP.

KW morphogenic; osteogenic protein; developmental cascade; OP-2;

KW inflammatory; anti-inflammatory; Transforming Growth Factor;

KW TGF-beta super-family; hippocampus.

OS Homo sapiens.

Key

Location/Qualifiers

FT protein 264..402

FT /note= "contains conserved 7 cysteine skeleton"

PN W09304692-A.

PD 18-MAR-1993.

PF 28-AUG-1992; U07358.

PR 30-AUG-1991; US-752764.

PR 30-AUG-1991; US-752861.

PR 30-AUG-1991; US-753059.

PA (CREA-) CREATIVE BIOMOLECULES INC.

Cohen CM, Kubarsampath T, Oppermann H, Ozkaynak E;

Pang RHL, Rueger DC, Smart JE;

WPI: 93-100652/12.

DR N-PSDB, Q38735.

PT Morphogen-induced modulation of inflammatory response - and

resulting tissue damage, e.g. in autoimmune diseases, diabetes,

asthma, ischemia reperfusion injury, etc.

Claim 26; Page 121-123; 16pp; English.

Human osteogenic protein (OP)-2 is a preferred morphogen for use in treating tissue damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.

Proteins having at least 70% homology with OP-2 amino acid

sequences can also be used. See R33400 for mature OP-2.

Sequence 402 AA;

Query Match 1.5%; Score 125; DB 6; Length 402;  
 Best Local Similarity 39.7%; Pred. No. 1.45e+00;

Matches 25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;

Db 12 glalcalggggpqrppp-gc-pqrllg-arerrdvgrellavlgpgr-prprappaas 67

Qy 172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASR 230

Db 68 rlp 70

231 SLP 233

PT	AC	W00238;
PS	DT	21-NOV-1996 (first entry)
CC	DE	Human osteogenic protein OP-2.
CC	KW	Morphogen; osteogenic protein; dentine; tooth decay; caries;
CC	KW	morphogenesis; odontoblast; OP-2.
CC	OS	Homo sapiens.
CC	FH	Location/Qualifiers
CC	Key	1..17
CC	FT	/label= sig_peptide
CC	FT	18..263
SQ	FT	region
Sequence	FT	/label= Pro_region
402 AA;	FT	264..402
Query Match	FT	/label= Mat_protein
Best Local Similarity	FT	301..402
Matches	FT	/label= 7-Cys_C-terminal_domain
25;	FT	
Conservative	FT	
12;	FT	
Mismatches	FT	
21;	FT	
Indels	FT	
5;	FT	
Gaps	FT	
5;	FT	
Query	FT	
172	FT	
GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASR	FT	
Db	PN	W0926777-61.
68	PD	06-SEP-1996.
rlp	PF	14-FEB-1996.
70	PR	01-MAR-1995; US-3166930.
	PA	(CREA-) CREATIVE BIOMOLECULES INC.
	PI	Charette MF, Ruthard RB;
	DR	WPI: 96-412583/41.
	DR	N-PSDB; T33443.
	DR	DR
	PS	Use of morphogen(s), e.g. osteogenic proteins, on dentinal surfaces
	PT	- for inducing dentine morphogenesis, desensitising teeth or sealing
	PT	tooth cavities
	PT	Disclosure; Page 58-59; 106pp; English.
	PS	Human hippocampus full-length osteogenic protein OP-2 (W00238)
	CC	includes a pro-sequence and the morphogenically active mature
	CC	protein sequence (see also W00223) that includes a 7-Cys C-terminal
	CC	domain. OP-2 can be expressed from intact or truncated cDNA
	CC	(T33443) in prokaryotic or eukaryotic host cells. Mature OP-2 and
	CC	other morphogens (see also W00221-35). Partic. human OP-1 (W00221),
	CC	can be used to induce dentine morphogenesis to seal dental cavities
	CC	and to desensitise teeth to pressure and/or temp.
	SQ	Sequence 402 AA;
	Query Match	1..5%; Score 125; DB 19; Length 402;
	Best Local Similarity	39.7%; Pred. No. 1.45e+00;
	Matches	25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;
	Db	12 glalcalggggpqrppp-gc-pqrllg-arerrdvgrellavlgpgr-prprappaas 67
	Qy	172 GPPLYQLGAAATQA-RPPHASGPRRLGCERAWNHSREAGYPLGLPAPGARRGGSASR 230
	Db	68 rlp 70
	Qy	231 SLP 233
	RESULT	13
	ID	R47292 standard; Protein: 402 AA.
	AC	
	DT	02-SEP-1994 (first entry)
	DE	hOP-2.
	KW	Human; hippocampus; osteogenic protein; OP-1; hOP-1; mature; injury;
	KW	survival; neural cell; morphogen; chemical; mechanical; neuropathy;
	KW	transected nerves; demyelinated cell; toxin; ethanol; Parkinson's;
	KW	Alzheimers; Huntington's chorea; amyotrophic lateral sclerosis;
	KW	multiple sclerosis; neoplastic lesion; central nervous system; CNS;
	KW	retinoblastoma; glial cell neoplasm; redifferentiation; neuroblastoma;
	KW	peripheral nervous system; neurite; outgrowth; cell aggregation;
	KW	cell adhesion; axonal; nerve regeneration; vascularisation;
	KW	myelin sheath.
	OS	Homo sapiens.
	PN	W09403200-A.
	PD	17-FEB-1994.
	PF	29-JUL-1993; U07189.
	PR	31-JUL-1992; US-922813.
	PR	04-MAR-1993; US-039335.
	PR	31-MAR-1993; US-040510.
	PA	(CREA-) CREATIVE BIOMOLECULES INC.
	PI	Jones WK, Kuberanapath T, Oppermann H, Ozkaynak E;

RESULT 12  
 ID W00238 standard; Protein: 402 AA.

12  
 ID W00238 standard; Protein: 402 AA.

PI	Rueger DC, Tucker RF;
DR	WPI: 94-065399/08 .
DR	N-PSDB; Q56333.
PT	Use morphogens to improve survival of neural cells - also stimulating re-differentiation in transformed cells and prodn. of adhesion molecules, for treating traumatic injury, neuropathy and nerve cell cancers, etc.
PT	Claim 23: Page 131-134; 176pp; English.
CC	This sequence represents the human hippocampus derived protein, osteogenic protein, hop-2. The mature Op-1 protein was used in the method of the invention for improving survival of neural cells. Morphogens such as this, can be used to treat (protect) cells which have suffered chemical or mechanical injury, eg. transected nerves; demyelinated cells; cells exposed to toxins such as ethanol, and cells at risk because of neuropathies (such as Parkinsons and Alzheimers disease; Huntington's chorea; amyotrophic lateral sclerosis or multiple sclerosis), or because of neoplastic lesions (esp. retinoblastoma or glial cell neoplasms). At risk cells can be in the central or peripheral nervous systems. When used to induce redifferentiation, morphogens such as this, are used to treat neurite outgrowth, cell aggregation and/or cell adhesion. These Proteins stimulate complete axonal nerve regeneration, including vascularisation and reformation of the myelin sheath. Nerves can be regenerated over long distances, eg. greater than 10mm.
CC	Induce formation of neurite outgrowth, cell aggregation and/or cell adhesion. These Proteins stimulate complete axonal nerve regeneration, including vascularisation and reformation of the myelin sheath. Nerves can be regenerated over long distances, eg. greater than 10mm.
SQ	Sequence 402 AA;
Query Match	1.5%; Score 125; DB 9; Length 402;
Best Local Similarity	39.7%; Pred. No. 1.45e+00;
Matches	25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;
Db	12 gialcalggggpqlrprrpp-gc-pqrllg-arerrdvgrelavlgipgr-prprappaas 67
Qy	172 GPPLYQLGATAQ-RPPHASGPRRLGCERAWNHSTREAGYPLGLPAPGARRGGASR 230
Query Match	1.5%; Score 125; DB 12; Length 402;
Best Local Similarity	39.7%; Pred. No. 1.45e+00;
Matches	25; Conservative 12; Mismatches 21; Indels 5; Gaps 5;
Db	68 rlp 70
Qy	231 SLP 233
RESULT	15
ID	R50200 standard; Protein: 402 AA.
AC	R50200;
DT	11-OCT-1994 (first entry)
DE	Human OP-2.
KW	OP-1; OP-2; CBMP2; Vg1(fx); Vgr(fx); DPP(fx); BMP6(fx); Gdf-1(fx); 60A(fx); Bap3(fx); Bap5(fx); Bap6(fx);
KW	osteogenic protein; morphogen; morphogenic protein; gastrointestinal tract; luminal lining; epithelial cell; proliferation; ulcer; lesion; inflammation; regeneration; OS Homo sapiens.
PN	WO9406120-A.
PD	31-MAR-1994.
PF	15-SEP-1993; US-945286.
PR	15-SEP-1992; US-945286.
DR	04-MAR-1993; US-029335.
PR	31-MAR-1993; US-045110.
PA	(CREA-) CREATIVE BIOMOLECULES INC.
PI	Charette MF, Cohen CM, Kubera-Sampath T, Oppermann H;
PI	Ozkaynak E, Pang RHL, Rueger DC, Smart JE;
WP	94-118121/14.
PT	Maintaining integrity of gastrointestinal lining using a morphogen (stimulant) - for treating or preventing ulceration, also to inhibit endothelial cell proliferation and reduce side effects of cancer therapy.
PT	Claim 35-36; Page 111-113; 151pp; English.
PS	Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, BMP3(fx) and at least 80% homology with DPP(fx), GDF-1(fx), 60A(fx), Vgr(fx), Vg1(fx), BMP5(fx) and BMP6(fx) are useful for maintaining the integrity of the gastrointestinal tract luminal lining in a mammal, including (1) limiting epithelial cell proliferation, (2) inhibiting ulcerative lesion formation, (3) inhibiting inflammation normally associated with ulcerative diseases, and/or (4) stimulating the repair of ulcerative lesions and the regeneration of the luminal tissue.
SQ	Sequence 402 AA;
Query Match	1.5%; Score 125; DB 9; Length 402;
Best Local Similarity	39.7%; Pred. No. 1.45e+00;
DR	WPI: 94-324521/40.
DR	N-PSDB; Q72706.

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	Matches	25:	Conservative	12:	Mismatches	21:	Indels	5:	Gaps	5:
Db	12	g	lalcalggggplrppp	-gc-pqrllg-	aerrd	qrellavlg	lpgr-prprappaas	67		
Qy	172	GPPPLYOLGAATQA	-RPPPHASGP	RRLG	CERAWNH	SYREAGVPLGLPAPGARRGGSASR	230			
Db	68	r1P	70							
Qy	231	SLP	233							

Search completed: Thu Jul 30 14:44:41 1998  
Job time : 102 secs.







Query Match 1.6%; Score 132; DB 2; Length 317;  
Best Local Similarity 26.4%; Pred. No. 7.5e-03;  
Matches 39; Conservative 38; Mismatches 64; Indels 7; Gaps 6;

RESULT 7

ENTRY S16681 #type complete  
TITLE homeotic protein - human  
ORGANISM Homo sapiens #common\_name man  
DATE 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
17-Oct-1997

ACCESSIONS S16681

REFERENCE Deguchi, Y.; Kehrl, J.H.  
Nucleic Acids Res. (1991) 19:3742  
Nucleotide sequence of a novel diverged human homeobox gene  
encodes a DNA binding protein.  
#cross-references MUID:91305125

accession S16681 Preliminary; nucleic acid sequence not shown;  
status preliminary; nucleic acid sequence not shown

#molecule\_type mRNA  
#residues 1-316 #label DEG  
#cross-references EMBL:X65537

#note the nucleotide sequence was submitted to the EMBL Data  
Library, January 1991  
#superfamily unassigned homeobox proteins; homeobox homology  
DNA binding; homeobox; nucleus; transcription regulation

CLASSIFICATION #domain homeobox homology #label HOX  
KEYWORDS  
FEATURE 73-127 #domain homeobox homology #label HOX  
SUMMARY #length 316 #molecular\_weight 34773 #checksum 3095

Query Match 1.6%; Score 136; DB 2; Length 316;  
Best Local Similarity 30.9%; Pred. No. 2.43e-03;  
Matches 21; Conservative 20; Mismatches 24; Indels 3; Gaps 3;

Db 202 RPWSTASSDCSYGRGIAPRGEAT-SPRPSRSPPAODRSRPARSAPPAASGGAWTH 260  
Qy 201 RAWHNSVREAGY-PLGLPAPGARRGGASASRLPLPKRPRRG-AAPPERFTYVGQGSWAH 258

Db 261 PARPREQA 268  
Qy 259 PGTRRGPS 266

RESULT 8

ENTRY A28996 #type complete  
TITLE Proline-rich Protein M14 precursor - mouse  
ORGANISM Mus musculus #common\_name house mouse  
DATE 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change  
20-Mar-1998

ACCESSIONS A28996

REFERENCE Ann, D.K.; Smith, K.; Carlson, D.M.  
J. Biol. Chem. (1988) 263:10887-10893  
Molecular evolution of the mouse proline-rich protein  
multigene family. Insertion of a long interspersed repeated  
DNA element.

#cross-references MUID:882273214  
#accession A28996  
#molecule\_type DNA  
#residues 1-317 #label ANN  
#cross-references GB:M23236; GB:J03891; NID:9200535; PID:9567232

GENETICS #introns 22/1  
CLASSIFICATION #superfamily proline-rich protein  
KEYWORDS saliva  
FEATURE 1-15  
16-317  
#domain signal sequence #status predicted #label SIG  
#product proline-rich protein M14 #status Predicted  
#label MAT

SUMMARY #length 317 #molecular\_weight 31719 #checksum 8454

Query Match 1.6%; Score 137; DB 2; Length 628;  
Best Local Similarity 25.0%; Pred. No. 1.82e-03;  
Matches 73; Conservative 64; Mismatches 134; Indels 21; Gaps 20;

Db 157 GPWLTTKTPRTSYVRQPRSAATRGPSPFRPLILLPKV-VH-WHDDDPHSSLRPRGSRSSRLQLQPT 214  
Qy 172 GPPLYQLGAATQARPPHAS-GPR-RRIGCERAWNHSYREAGYPLGLPAPGAR-RR-GGS 227

Db 215 VRPILLAFNOFHSPRQPPPLSDPGIILGPRLPHSTPDRPPRPI-TGPSN-THDLRPL 272  
Qy 228 ASRSLPLEKRPKRGAAPPERTPVG-QGSWAH-HPGRTRGPDSDRGFCVTPSPARAEATSL 285

Db 273 SVLPRTSPRGRGLIPNPNNRHRSTGHTIPPTTSRPTGPPSRQLRQPVH-LYQSSPHTPNFPRP 331  
Qy 286 EG-ALSGRNRHSHPSVGRQHAGPSPSTSPRPREWDTPCPVYATEKHKHY-SSSGDKEQIRP 343

Db 332 SSTRKDALQLTGPRGHIERLQSPANERTSERSPPTRKLPRSESEPNLPKLPLEPTALAP 391  
Qy 344 SFL-SFL-SSU-R-PSLTGARRLVETIFLGSRPMPGTTRRLPRPQRYWQMRPFLELLG- 398

Db 392 SYTRRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPMPRRL 442  
Qy 399 NHAQC-PYGVLLKTHCPFLRA-AVTPANGVCAREKQPGSVAPEEEDTDPRRL 448

RESULT 10

ENTRY S27923 #type complete  
TITLE Gene LF3 protein - human herpesvirus 4  
ORGANISM #formal\_name human herpesvirus 4  
DATE 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change  
08-Sep-1997

ACCESSIONS S27923  
REFERENCE



```

ORGANISM          # formal_name Orf virus
DATE             23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
ACCESSIONS       31-Oct-1991
#authors         Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
#journal        Virology (1990) 176:379-389
#title          Sequence analysis of the inverted terminal repetition in the
#cross-references MUID:9026654
#accession       D34768
##status        preliminary
##molecule-type DNA
##residues       1-264 #!label FRA
##cross-references GB:MB30023; EMBL:M37623; PID:g332561; checksum 1957
SUMMARY          #length 264 #molecular_weight 25613 #checksum 1957

Query Match      1.5%; Score 129; DB 2; Length 264;
Best Local Similarity 28.2%; Pred. No. 1.74e-02;
  matches 33; Conservative 40; Mismatches 37; Indels 7; Gaps 5;
Db   150 RAPGRAGRYPARPAASAAASRRHGPAAARSSPAABRAPPRAAAPPRAASS-GS 208
Qy   201 RAWNNSVPRRGVPVLGLPAPARRGGSSARSPLPKRP---R-RGAPEPERTPVQGS 255

Db   209 RASSGPPRRAARS-SAASGSRPAASGPARAAPAASSARTSAGEAARGPGAPRAGW 264
Qy   256 WAHPGRTGRPSDRGFcvVSPARPAEATSEALSGTRSHSPVGRHAGPPTSR 312

RESULT          1.5
ENTRY           S19560 #type complete
TITLE           PROLINE-rich protein MP4 - mouse
ORGANISM        #formal_name Mus musculus #common_name house mouse
DATE            22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS      20-Mar-1998
REFERENCE        S19560
#authors         Roberts, S.G.E.; Layfield, R.; Bannister, A.J.; McDonald,
#journal        C.J. Eur. J. Biochem. (1991) 202:969-974
#title          Gene sequence of mouse B-type proline-rich protein MP4.
#cross-references MUID:92111548
#accession       S19560
##status        Preliminary
##molecule-type DNA
##residues       1-300 #!label ROB
##cross-references GB:X58438; PID:953182
REFERENCE        S22570
#authors         Roberts, S.G.E.; Layfield, R.; McDonald, C.J.
#journal        Nucleic Acids Res. (1991) 19:5205-5211
#title          The mouse proline-rich protein MP6 promoter binds
#cross-references MUID:92020206
#accession       S22570
##molecule-type DNA
##residues       1-14 #!label RO2
##cross-references EMBL:461126
CLASSIFICATION  #superfamily Proline-rich protein
SUMMARY          #length 300 #molecular_weight 31129 #checksum 8443

Query Match      1.5%; Score 131; DB 2; Length 300;
Best Local Similarity 25.2%; Pred. No. 9.98e-03;
  matches 34; conservative 40; Mismatches 54; Indels 7; Gaps 7;
Db   131 PGNQGCPPPG-GPQQRPP-QPGNQGPPPGPQQRPQPGPQGNQGPP--QCGPHP-P-PR 186
Qy   180 AAATQARPPIASGPRRLGCERAWNNSVREANGVPLGPAPGARRGGSAASRLPLKRPR 239

Db   187 PGNQGCPPPG-GPQQRPP-QPGNQGPPQGPQQGGG--POAPPRRPGNQGPPQGPQQGGG-POAPPRRPGNQGPPQGPQQGGG 245

```



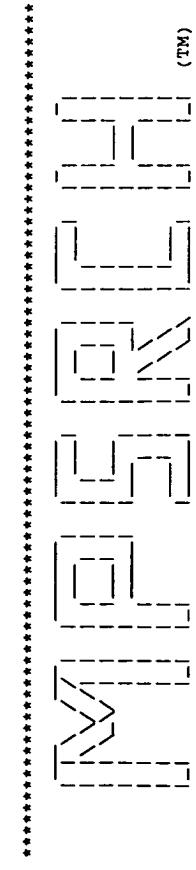
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)		
DE	SALIVARY PROLINE-RICH PROTEIN PO (ALLEL M) (CONTAINS: PEPTIDE P-D)		
DE	(FRAGMENT).		
PRB4.			
GN	HOMO SAPIENS (HUMAN).		
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
OC	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE: B9121439.		
RA	LYONS K.M.; STEIN J.H.; SMITHIES O.;		
RA	GENETICS 120:255-265 (1988).		
RL	[2]		
RN	SEQUENCE OF 165-234.		
RX	MEDLINE: B3186122.		
RA	SAITO E.; ISEMIURA S.; SANADA K.;		
RJ	J. BIOCHEM. 93:445-502 (1983).		
RL	EMBL: X07704.; E225547.; -.		
DR	A03295; PIHUSD; -.		
DR	PIR; S03175; S03175.		
DR	HSSP; P19999; 1CLG.		
DR	MIM: 168730; -.		
DR	MM: 180990; -.		
KW	REPEAT; PAROTID GLAND; SALIVA; MULTIGENE FAMILY.		
FT	NON TER 1 1		
FT	CHAIN 165 234 AA; 23676 MW; ED2D4ADC CRC32;		
SQ	SEQUENCE 234 AA; 23676 MW; ED2D4ADC CRC32;		
Query Match	1.8%; Score 150; DB 1; Length 234;		
Best Local Similarity	29.3%; Pred. No. 4.42e-07;		
Matches	43; Conservative 41; Mismatches 53; Indels 10; Gaps		
Db	88 GPPP-OGQNQSGQ-PPPHGKPRPPP-QGG-NOSHRPPPPP-QKPER-PPPOQGNQSQQ 14		
Qy	172 GPPLQLQIQAQARPPPHASGRPLRGKERAWSVRAVGVLPGLPAPARRGQSASRS 23		
Db	142 -P-PPHPGKPEGPPQGPNKSRARSPPKGQPGQGPQOEGNKPQOGPPPPGGN 19		
Qy	232 LPLPKRERGAAPEPERTPVGQDSWAHGRTRGSDR-GFCVYSPARPAE-EAITLEGAL 28		
Db	200 PQQPQAPPAGKRDQGPPPPQGGRPPR 226		
Qy	290 SGTRSHSPSVGRHQHAGPPSTSRPVRP 316		
RESULT	3 ATIN HSVBP STANDARD; PRT; 504 AA.		
RP	P30020; SEQUENCE FROM N.A.		
RA	01-APR-1993 (REL. 25, CREATED)		
RA	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)		
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)		
DE	ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).		
OS	BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).		
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RX	MEDLINE: 93012995.		
RA	CARPENTER D.E.; MISRA V.;		
RJ	Gene 119:259-263(1992).		
CC	- FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF IMMEDIATE-		
CC	EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).		
CC	- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING PROTEIN.		
DR	Z11610; E26449; -.		
DR	S24229; S24229.		
DR	PIR; JC1306; JC1306.		
KW	TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING		
SQ	SEQUENCE 504 AA; 54028 MW; 79F42020 CRC32;		
Query Match	1.8%; Score 153; Pred. No. 1.43e-07;		
Best Local Similarity	31.3%; Mismatches 33; Indels 12; Gaps		
Matches	.46; Conservative 33; Mismatches 56; Indels 12; Gaps		





FT DOMAIN	256	318	COILED COIL (8 HEPTADS).
FT DOMAIN	419	432	COILED COIL (2 HEPTADS).
FT DOMAIN	440	509	COILED COIL (10 HEPTADS).
FT DOMAIN	298	318	LEUCINE-RICH REPEATS.
FT REPEAT	298	304	LRR 1.
FT REPEAT	305	311	LRR 2.
FT REPEAT	312	318	LRR 3.
SQ SEQUENCE	566 AA:	61970 MW;	7A421F03 CRC32;
Query Match	1.2	Score 127; DB 1; Length 566;	
Best Local Similarity	35.7%	Pred. No. 1.60e-03; Indels 5; Gaps 5;	
Matches 30;	Conservative 19;	Mismatches 30;	
Db 34 SARGTDRVGSVARARPPSPQGPQRGAVKTAQRPGVHGGGLRTGPTSRCQDPSARAKLPS 93	Qy 217 PAPGARRGGSAARSRLPKRPRGAADEPERTPV-GGSWAHPGRTRGSPDSRGFCVYSP 275	Qy 217 PAPGARRGGSAARSRLPKRPRGAADEPERTPV-GGSWAHPGRTRGSPDSRGFCVYSP 275	
Db 94 VTRGAFLPPPSGK-HGLGGTSSH 116	Qy 273 VSPARPAEATSLLEGALSGTRSH 296	Db 142 SPPSPSPTDPSPSPSPTDPSPSPSPTDPSPSPSPTDPSPSPSPLGDMYFSS 201	
Db 95 VTRGAFLPPPSGK-HGLGGTSSH 116	Qy 276 ARPAEEATSLLEGALSGTRSHPSVGRQHAGP-PSTSPRPRPMDTCPCPVYAETKHFLYS 334	Qy 276 ARPAEEATSLLEGALSGTRSHPSVGRQHAGP-PSTSPRPRPMDTCPCPVYAETKHFLYS 334	
RESULT 12 MIAE SALTY STANDARD: PRT; 270 AA.	RESULT 14 ID NOD1_RHSN STANDARD; PRT; 322 AA.	RESULT 14 ID NOD1_RHSN STANDARD; PRT; 322 AA.	RESULT 14 ID NOD1_RHSN STANDARD; PRT; 322 AA.
AC P08015;	AC P53359;	AC P53359;	AC P53359;
DT 01-OCT-1994 (REL. 30, CREATED)	DT 01-NOV-1997 (REL. 35, CREATED)	DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)	DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)	DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)	DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	DE NODULATION PROTEIN D 1 (NOD1) OR Y4A1.
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)	DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	DE NODULATION PROTEIN D 1 (NOD1) OR Y4A1.	OS RHIZOBIUM SP. (STRAIN NGR234).
DE tRNA-(MS(2)U(6)A)-HYDROXYLASE (EC 1.12.1.1)	DE NODULATION PROTEIN D 1 (NOD1) OR Y4A1.	OS PLASMID SYM_PNGR234A.	OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; RHIZOBIAEAE.
GN MIAE.	GN NOD1 OR Y4A1.	OC PLASMID SYM_PNGR234A.	OC PLASMID SYM_PNGR234A.
OS SALMONELLA TYPHIMURIUM.	OS RHIZOBIUM SP. (STRAIN NGR234).	OS RHIZOBIUM SP. (STRAIN NGR234).	OS RHIZOBIAEAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.
[1]	[1]	[1]	[1]
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RP STRAIN-T2;	RP STRAIN-T2;	RP STRAIN-T2;	RP STRAIN-T2;
RC MEDLINE; 94075212	RC MEDLINE; 94075212	RC MEDLINE; 97305956.	RC MEDLINE; 97305956.
RX RA PERSSON B.C., BJOERK G.R.;	RX RA PERSSON B.C., BJOERK G.R.;	RX RA PERRET X.;	RX RA PERRET X.;
RJ J. BACTERIOL. 175:7776-7785 (1993).	RJ J. BACTERIOL. 175:7776-7785 (1993).	RJ NATURE 387:394-401 (1997).	RJ NATURE 387:394-401 (1997).
CC - FUNCTION: PRODUCTION OF THE MODIFIED NUCLEOSIDE 2-METHYLTHIO-CIS-RIBOZEATIN (MS(2)U(6)A) FOUND IN SOME TRNA'S. CATALYZES THE OXYGEN-DEPENDENT TRANSFORMATION OF MS(2)U(6)A INTO MS(2)U(6)A.	CC - FUNCTION: NOD1 REGULATES THE EXPRESSION OF THE NOD ABOVE GENES WHICH ENCODE OTHER NODULATION PROTEINS. NOD1 IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.
CC - PATHWAY: THIRD STEP OF SYNTHESIS OF 2-METHYLTHIO-CIS-RIBOZEATIN.	CC - PATHWAY: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.
CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.	CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.	CC -1- SIMILARITY: BELONGS TO THE LISR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL; X73368; G31700; -.	EMBL; X73368; G31700; -.	DR E000005; G2182301; -.	DR E000005; G2182301; -.
PIR; S34361; S34361.	PIR; S34361; S34361.	DR PROSTATE; PS0044; HTH_LISR_FAMILY; 1.	DR PROSTATE; PS0044; HTH_LISR_FAMILY; 1.
STYGENE; SG10234; MIAE.	STYGENE; SG10234; MIAE.	KW NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR; KW REPRESSOR; MULTIGENE FAMILY; PLASMID.	KW NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR; KW REPRESSOR; MULTIGENE FAMILY; PLASMID.
OXIDOREDUCTASE; tRNA PROCESSING.	OXIDOREDUCTASE; tRNA PROCESSING.	FT DNA_BIND 23 42 H-T_H_MOTIF (BY SIMILARITY).	FT DNA_BIND 23 42 H-T_H_MOTIF (BY SIMILARITY).
SEQUENCE 270 AA; 31140 MW;	SEQUENCE 270 AA; 31140 MW;	SEQUENCE 322 AA; 36460 MW;	SEQUENCE 322 AA; 36460 MW;
C528DEF2 CRC32;	C528DEF2 CRC32;	FAS23BEE CRC32;	FAS23BEE CRC32;
Query Match	1.3 ID Y091_NPVP STANDARD; PRT; 279 AA.	Query Match	1.4 ID P0280 STANDARD; PRT; 331 AA.
Best Local Similarity	1.4% Score 116; DB 1; Length 270; Pred. No. 5.84e-02; Indels 2; Gaps 2;	Best Local Similarity	1.4% Score 121; DB 1; Length 322; Pred. No. 1.17e-02; Indels 7; Gaps 7;
Matches 16;	Matches 13; Mismatches 14; Indels 2; Gaps 2;	Matches 28;	Matches 23; Mismatches 35; Indels 7; Gaps 7;
Db 15 LRMNYQIQLSPVLNFHLCHPTPOAW-IYQARDPQNLLPLTLHDLC 58	Db 101 -I-LSDMTLMLPVERVVRAREAPYSFELL 131	Db 101 -I-LSDMTLMLPVERVVRAREAPYSFELL 131	Db 101 -I-LSDMTLMLPVERVVRAREAPYSFELL 131
Qy 14 LRSHYREV-PLATEYRRLQGQWLRYQRGDPAAFRALVAQQLYC 57	Qy 73 QVSCLKELVARY-LQRLCEGAKNVLAQGFALL 104	Qy 73 QVSCLKELVARY-LQRLCEGAKNVLAQGFALL 104	Qy 73 QVSCLKELVARY-LQRLCEGAKNVLAQGFALL 104
RESULT 13 ID P01341; STANDARD; PRT; 279 AA.	RESULT 15 ID PR01_HUMAN STANDARD; PRT; 331 AA.	RESULT 15 ID PR01_HUMAN STANDARD; PRT; 331 AA.	RESULT 15 ID PR01_HUMAN STANDARD; PRT; 331 AA.
AC 01-NOV-1997 (REL. 35, CREATED)	AC P0280;	AC P0280;	AC P0280;
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	DT 20-MAR-1987 (REL. 04, CREATED)	DT 20-MAR-1987 (REL. 04, CREATED)	DT 20-MAR-1987 (REL. 04, CREATED)
OS ORYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNIV).	OS ORYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNIV).	OS ORYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNIV).	OS ORYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNIV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRIDAE.	VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRIDAE.	VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRIDAE.	VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRIDAE.
[1]	[1]	[1]	[1]
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
AHRENS C.A., RUSSELL R.R., FUNK C.J., EVANS J., HARWOOD S.,	ROHRMANN G.F.,	ROHRMANN G.F.,	ROHRMANN G.F.,
VIROLOGY 229:381-399 (1997).	SAUVE PROLINE-RICH PROTEIN PRECURSOR (CONTAINS: BASIC PEPTIDE IB-6, DE PEPTIDE P-1) (CLONES CB3, CP4 AND CP5).	SAUVE PROLINE-RICH PROTEIN PRECURSOR (CONTAINS: BASIC PEPTIDE IB-6, DE PEPTIDE P-1) (CLONES CB3, CP4 AND CP5).	SAUVE PROLINE-RICH PROTEIN PRECURSOR (CONTAINS: BASIC PEPTIDE IB-6, DE PEPTIDE P-1) (CLONES CB3, CP4 AND CP5).

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Release 3.1A John F. Collins, Biocomputing Research Unit.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 30 14:49:07 1998; MesPar time 50.56 Seconds  
942.752 Million cell updates/sec

Title: >US-08-912-951-2  
(1-1132) from US08912951.PEP

Description: 8465  
Perf Score: 1  
Sequence: 1 MPRAPRRAVRSLSRSYRE.....TALEAAANPALPSDFKTIID 1132

Scoring table: PAM 150  
Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

sptrembl5  
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal  
5:sp\_mic 6:sp\_oranelle 7:sp\_phage 8:sp\_plant  
9:sp\_bacteria 10:sp\_risk 11:sp\_virus 12:sp\_vertebrate  
13:sp\_unclassified

Statistics: Mean 53.898; Variance 101.765; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Match Length DB ID Description Pred. No.

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	8465	100.0	1132	2	014746 TELOMERASE REVERSE TRA	0.0e+00
2	8459	99.9	1132	2	014783 TELOMERASE CATALYTIC S	0.0e+00
3	678	8.0	988	1	013339 TELOMERASE REVERSE TRA	6.18e-110
4	681	8.0	989	1	013338 TELOMERASE SUBUNIT P12	1.42e-110
5	439	5.2	1031	3	00939 TELOMERASE CATALYTIC S	3.85e-60
6	439	5.0	67	10	035432 CHROMOSOME XII COSMID	4.19e-57
7	314	3.7	884	1	006163 PAROTID 'O' PROTEIN (F	2.25e-35
8	142	1.7	234	2	000650 IS 1222 GENE ORF-A AND	3.44e-05
9	141	1.7	276	9	HYPOTHETICAL 60.2 KD P	4.83e-05
10	147	1.7	296	11	069118 LF3 PROTEIN	6.21e-05
11	143	1.7	574	13	ACTIN ASSOCIATED PROTE	2.45e-05
12	136	1.6	316	2	HOMEBOX PROTEIN (FRAG	2.58e-04
13	132	1.6	317	10	PROLINE RICH PROTEIN P	9.59e-04
14	133	1.6	539	3	SIMILARITY TO COLLAGEN	6.92e-04
15	135	1.6	585	11	HYPOTHETICAL 60.2 KD P	3.59e-04
16	132	1.6	924	11	LF3 PROTEIN	9.59e-04
17	125	1.5	227	10	PROLINE RICH SALIVARY	9.02e-03
18	129	1.5	264	11	HOMOLOGUE OF RETROVIRAL	2.33e-03
19	131	1.5	300	10	PROLINE RICH PROTEIN N	1.33e-03
20	129	1.5	309	2	SALIVARY PROLINE-RICH	2.53e-03

RESULT	1	PRELIMINARY;	PRT;	1132 AA.
ID	014746			
AC	014746;			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DE	TELOMERASE REVERSE TRANSCRIPTASE.			
GN	HTRT;			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-KIDNEY;			
RA	NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H., LINGNER J., HARVEY C.B., CZECH T.R., RYL SCIENCE 277:955-959 (1997).			
RL	AFO15930; G2330017; EMBL; AF015930; G2330017.			
DR	RNA-DIRECTED DNA POLYMERASE.			
KW	SEQUENCE 1132 AA; 126996 MW; 2DFBEDF3 CRC32;			
SQ	Query Match 100.0%; Score 8465; DB 2; Length 1132; Best Local Similarity 100.0%; Pred. No. 0.0e+00; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

## ALIGNMENTS

21 123 1.5 403 2 015220 PRPL-2 PROTEIN (FRAGME  
22 123 1.5 439 8 0424220 CHITINASE PRECURSOR.  
23 124 1.5 464 8 041645 EXTENSIN (FRAGMENT).  
24 125 1.5 501 2 099958 MESENCHYME FORK HEAD-1  
25 128 1.5 527 9 053913 BETA-KETOACYL SYNTHASE  
26 130 1.5 1236 9 006264 HYPOTHETICAL 131.9 KD  
27 126 1.5 3247 11 065553 UL36.  
28 115 1.4 106 11 041981 HYPOTHETICAL 9.9 KD PR  
29 117 1.4 197 3 Q17626 COG2.8.  
30 118 1.4 203 3 P91497 CODED FOR C. ELEGAN  
31 115 1.4 203 3 P91028 CODED FOR BY C. ELEGAN  
32 118 1.4 236 11 Q85028 SUBSTRATE OF THE PROTE  
33 115 1.4 260 10 Q64306 PROLINE-RICH PROTEIN  
34 116 1.4 295 10 Q07611 PROLINE-RICH PROTEIN  
35 116 1.4 297 2 Q16038 PROLIM PROTEIN (FRAGME  
36 118 1.4 322 9 Q53180 MPK3030 NODDI GENE IN  
37 115 1.4 340 11 Q15194 HYA22.  
38 115 1.4 358 2 Q08805 SALIVARY PROLINE-RICH  
39 115 1.4 382 2 Q00599 CON1.  
40 116 1.4 488 8 Q04528 SEQUENCE OF BAC F20P5  
41 118 1.4 526 11 Q85027 VIRAL PROTEINASE.  
42 122 1.4 657 8 Q22835 SE16 ISOLOG.  
43 114 1.3 185 11 Q39738 ORF 1 PROTEIN.  
44 114 1.3 301 10 Q62105 31-KDA PROLINE-RICH SA  
45 114 1.3 373 1 Q03787 HYPOTHETICAL 43.8 KD P

RESULTS

1  
ID 014746  
AC 014746;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DE TELOMERASE REVERSE TRANSCRIPTASE.

GN HTRT;  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-KIDNEY;  
RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H., LINGNER J., HARVEY C.B., CZECH T.R., RYL SCIENCE 277:955-959 (1997).  
RL AFO15930; G2330017; EMBL; AF015930; G2330017.  
DR RNA-DIRECTED DNA POLYMERASE.  
KW SEQUENCE 1132 AA; 126996 MW; 2DFBEDF3 CRC32;

Db	301	ROHHAGPPSTSRRPWRDTPCPVVYAEKTHFLYSSGDEQLRPSFLSSLRPLTGARRL	360	RA	BACCHETTI S., HABER D.A., WEINBERG R.A.;
Qy	301	RQHAGGPSTSRRPWRDTPCPVVYAEKTHFLYSSGDEQLRPSFLSSLRPLTGARRL	360	RL	CELL 90-785-795 (1997);
DR				EMBL; AF018167; G2347129;	
SEQUENCE	1132 AA;	126938 MW;	C1EE2AF CRC32;		
Query Match	99.9%	Score 8459;	DB 2;	Length 1132;	
Best Local Similarity	99.9%	Pred. No. 0.00e+00;			
Matches	1131; Conservative	0; Mismatches	1;	Indels 0; Gaps 0;	
Db	1	MPPAPRCRAVSLRSIYREVILPLATEVRLGPGQWLVRQGDPAATRALVAQCLVCPW	60		
Qy	1	MPPAPRCRAVSLRSIYREVILPLATEVRLGPGQWLVRQGDPAATRALVAQCLVCPW	60		
Db	61	DARPPAAPSFRQVSCLKEIYARVLRQICERGAKNVLAQFGLDARGGPPEAFTTSVR	120		
Qy	61	DARPPAAPSFRQVSCLKEIYARVLRQICERGAKNVLAQFGLDARGGPPEAFTTSVR	120		
Db	121	SYLPNVTIDALRGSGANGLLLRVGDVDYLVLARCAFLVYLAPSCAYQVGPPLYLGA	180		
Qy	121	SYLPNVTIDALRGSGANGLLLRVGDVDYLVLARCAFLVYLAPSCAYQVGPPLYLGA	180		
Db	181	AHQARPPIHASGPGRRIUGCERAWNHSTREAGYPLGLPAPGARRGGASRSPLPKPRR	240		
Qy	181	AHQARPPIHASGPGRRIUGCERAWNHSTREAGYPLGLPAPGARRGGASRSPLPKPRR	240		
Db	241	GAAPEPERTPVQGGSWAHPGRGSDRGFCVSPARPAEETSLEGALSTRHSHPSVG	300		
Qy	241	GAAPEPERTPVQGGSWAHPGRGSDRGFCVSPARPAEETSLEGALSTRHSHPSVG	300		
Db	301	RQHAGGPPSTSRRPWRDTPCPVVYAEKHFLYSSGDEQLRPSFLSLRPSLTGARRL	360		
Qy	301	RQHAGGPPSTSRRPWRDTPCPVVYAEKHFLYSSGDEQLRPSFLSLRPSLTGARRL	360		
Db	361	VETIFLGSRPWMGTPTRPLRPLQRYQMRPLFELIGNHAQCPYGYLTKTCPLRAVT	420		
Qy	361	VETIFLGSRPWMGTPTRPLRPLQRYQMRPLFELIGNHAQCPYGYLTKTCPLRAVT	420		
Db	421	PAAGVCAREKPQGSVAAPEEEDDPRLVQLLRQHSSPQWQVGFVRACRLRPLQYQMLGWS	480		
Qy	421	PAAGVCAREKPQGSVAAPEEEDDPRLVQLLRQHSSPQWQVGFVRACRLRPLQYQMLGWS	480		
Db	481	RINERRFLRNTKKFISLGKAHSQELTWNMSVRGGCAWLRSRSPGVYCPVAEHLRREEI	540		
Qy	481	RINERRFLRNTKKFISLGKAHSQELTWNMSVRDCAWLRSRSPGVYCPVAEHLRREEI	540		
Db	541	LAKFLHNTMSYYVELLRSFFYTFETEQKRNLFYFKSWSKLSQISGIRQLKRYLRE	600		
Qy	541	LAKFLHNTMSYYVELLRSFFYTFETEQKRNLFYFKSWSKLSQISGIRQLKRYLRE	600		
Db	601	LSEAEVROHREARPALLTSRLRIPKPDGLRPNVMDYVVGARTFREKRAERLTSRVKA	660		
Qy	601	LSEAEVROHREARPALLTSRLRIPKPDGLRPNVMDYVVGARTFREKRAERLTSRVKA	660		
Db	661	LFSVLNTERARRGGLGSVGLDDDIHRAWRFTFLVYRAQDPPPELYFVKVDTVGAYDTI	720		
Qy	661	LFSVLNTERARRGGLGSVGLDDDIHRAWRFTFLVYRAQDPPPELYFVKVDTVGAYDTI	720		
Db	721	PODRLETVIASIKPONTYCVRAYQAAHGHVRAKFHKSHVSTLDLQPMRQFYAHL	780		
Qy	721	PODRLETVIASIKPONTYCVRAYQAAHGHVRAKFHKSHVSTLDLQPMRQFYAHL	780		
Db	781	QETSPRDAVVTEQSSLNEASGLFDYFLRMCHHAVRICKSYTQCQGTPQGSTLSTL	840		
Qy	781	QETSPRDAVVTEQSSLNEASGLFDYFLRMCHHAVRICKSYTQCQGTPQGSTLSTL	840		
Db	841	LCSLCYGDMENTKLAGIRRDGLLRLYDDELLPTPHTHAKTFLRTLVYRGAFCVYNL	900		
Qy	841	LCSLCYGDMENTKLAGIRRDGLLRLYDDELLPTPHTHAKTFLRTLVYRGAFCVYNL	900		
Db	901	RKTYYNPVEDEAQGTAFVQMPAHGLPWCCLLDRTTLEYQSDYSSYARTSIRASLTF	960		
Qy	901	RKTYYNPVEDEAQGTAFVQMPAHGLPWCCLLDRTTLEYQSDYSSYARTSIRASLTF	960		
Db	961	NRGFKAGRNMKRLKGTYLRLICHSLFDLQNSLQTYCTNITYKILLQAYRFHACVYQLP	1020		
Qy	961	NRGFKAGRNMKRLKGTYLRLICHSLFDLQNSLQTYCTNITYKILLQAYRFHACVYQLP	1020		
Db	1021	FHQQVKKNPFTFLRVSIDTASLICYSILKAKNAGMSLGAKGAGPLPSEAQNWLHQAFLL	1080		
Qy	1021	FHQQVKKNPFTFLRVSIDTASLICYSILKAKNAGMSLGAKGAGPLPSEAQNWLHQAFLL	1080		
Db	1081	KLTTRHRTVYPLLSRITAQTOSLRKLPGTTLTALEAAANPAPSDFTILD	1132		
Qy	1081	KLTTRHRTVYPLLSRITAQTOSLRKLPGTTLTALEAAANPAPSDFTILD	1132		
Db	1132	PRELIMINARY; PRT: 1132 AA.			
ID	014783	PRELIMINARY;	PRT:	1132 AA.	
AC	014783;				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DE					
GN					
HNST2.					
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAIORA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEYERSON M., COUTNER C.M., EATON E.N., ELLISEN L.W., STEINER P.,				
RA	CADDLE S.D., ZIAUGRA L., BEIJERSBERGEN R.L., DAVIDOFF M.J., LIU Q.,				
RA	RKTYYNPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLVEQSDYSSYARTSIRASLT				
Qy	901	RKTYYNPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLVEQSDYSSYARTSIRASLT	960		

961 NRGFKAGRMRKLFGVLRKCHSLFDLQVNSLQTVCNTIXYKILLQAYRFHACYVLQLP 1020  
 961 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
 Qy 961 NRGFKAGRMRKLFGVLRKCHSLFDLQVNSLQTVCNTIXYKILLQAYRFHACYVLQLP 1020  
 Db 1021 FHQQWKNPTEFLRVTSIDASICYSITSLKAKNAGMSLGAKGAAAGPLPSEAVQWLCHQAFL 1080  
 1021 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||  
 Qy 1021 FHQQWKNPTEFLRVTSIDASICYSITSLKAKNAGMSLGAKGAAAGPLPSEAVQWLCHQAFL 1080  
 Db 1081 KLTRHRVTVYLGLSRLTAQFQLSRKLPGTITLATEAANPALPSDEKTILD 1132  
 Qy 1081 KLTRHRVTVYLGLSRLTAQFQLSRKLPGTITLATEAANPALPSDEKTILD 1132  
 RESULT 3 PRELIMINARY; PRT; 988 AA.  
 ID 013339 AC 013339; DT 01-JAN-1998 (CREATED)  
 RC STRAIN=972H; RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,  
 RA LINGER J.J., HARLEY C.B., CECH T.R.;  
 RL SCIENCE 277: 955-959(1997).  
 DR EMBL; AF015783; G2340169;  
 KW RNA-DIRECTED DNA POLYMERASE,  
 SQ SEQUENCE 988 AA; 116328 MW; 39C385A7 CRC32;

Query Match Score 8.0%; Score 681; DB 1; Length 989;  
 Best Local Similarity 26.3%; Pred. No. 1.4e-110;  
 Matches 129; Conservative 136; Mismatches 204; Indels 21; Gaps 18;

Db 340 PNOVFAFLRSILVRFPKLIGNQRIFIEFLKLSRYESFLHYLMNSNIKISEI 399  
 Qy 458 PWQYGFVRACLRLVPGLWGSRHNERERFLNTKKTISLGRHAKLSQELTMWSVRDC 517  
 Db 400 EWLVGKRSNAMKCLSDFEKR-KQ-IFAEFYWLNSFIPLQSFFYITESSDLRNRTV 457  
 Qy 518 AWL--RRSPGVGCPAAEHLRREEILAKFLHWLMSVYVELRSFFVTTETFQRNLF 574  
 Query Match Score 8.0%; Score 678; DB 1; Length 988;  
 Best Local Similarity 26.4%; Pred. No. 6.18e-110; Indels 18; Gaps 15;  
 Matches 129; Conservative 133; Mismatches 208; Indels 18; Gaps 15;  
 Db 340 PNOVFAFLRSILVRFPKLIGNQRIFIEFLKLSRYESFLHYLMNSNIKISEI 399  
 Qy 458 PWQYGFVRACLRLVPGLWGSRHNERERFLNTKKTISLGRHAKLSQELTMWSVRDC 517  
 Db 400 EWLVGKRSNAMKCLSDFEKR-KQ-IFAEFYWLNSFIPLQSFFYITESSDLRNRTV 457  
 Qy 518 AWL--RRSPGVGCPAAEHLRREEILAKFLHWLMSVYVELRSFFVTTETFQRNLF 574  
 Query Match Score 8.0%; Score 678; DB 1; Length 988;  
 Best Local Similarity 26.4%; Pred. No. 6.18e-110; Indels 18; Gaps 15;  
 Matches 129; Conservative 133; Mismatches 208; Indels 18; Gaps 15;  
 Db 340 PNOVFAFLRSILVRFPKLIGNQRIFIEFLKLSRYESFLHYLMNSNIKISEI 399  
 Qy 458 PWQYGFVRACLRLVPGLWGSRHNERERFLNTKKTISLGRHAKLSQELTMWSVRDC 517  
 Db 400 EWLVGKRSNAMKCLSDFEKR-KQ-IFAEFYWLNSFIPLQSFFYITESSDLRNRTV 457  
 Qy 518 AWL--RRSPGVGCPAAEHLRREEILAKFLHWLMSVYVELRSFFVTTETFQRNLF 574  
 Db 458 YPRKDIWKLICRPETISMKAFAEKINENNYRMDTQ-KTLLPPAVRLPKKNTFRLLT 515  
 Qy 575 FVRKSWSKLSQSIGIROHLKRVQLRELSEAEYRQHREARPLTSRLRFIPKDGLRPIV 634  
 Db 516 NLRKFLIKQMGNSNK-KMLVSTNQTLRPAVASILKHLINEESSCIPN-LEVNMKLLFK 573  
 Qy 635 NM-D-YVYGARTERRERAERLTSRVKALFSVLYNEARRPGLGASVIGLDIHRMWT 692  
 Db 574 DLJKHMRMFRK-K-YFVRIDIKSCYDRIKQDLMFRYKKLKDPE-FVTKYATIH-ATS 629  
 Qy 693 FVLVRADOPPPBELYKVDTGAYDTIPQDRLETRIASIKRQNTIVCVRRTAVVQKAH 752  
 Db 630 DRATKNEVSSEASYFDAYPFK -WVQLLSMKT-SDFLFDYDWTKSSELFKMLKEH 686  
 Qy 753 GHVRKAKSHVSTLTDQPMQRFVHLQETSPLRDAVYIEQSSSLNEASSGLFDYFLRF 812  
 Db 687 LSHHVKGNSQWLVQKVGIPQGSILSSPLCHYMEDLDEYLSFTKRGSVLLRVDDDFL 746  
 Qy 813 MCCHAVERIGKSYVQOCGIPQGSILSILCSLCYGMENKLFAGIRDG-LLIRLVDDFL 871  
 Db 747 FITVNKKDAKKFLNLSLRGEFEKHNFESTSLEKTYVINFENSNGINNTFENESKRR-M-PFF 804  
 Qy 872 LVTPHFLHAKTFLRLTVRGPEYGCVVNLRKTVNNFPVEDALGGTAFVQMPAHGLEFWC 931  
 Db 805 GFSVNMRSID 814  
 Qy 932 GLLDDTRLE 941  
 RESULT 5 PRELIMINARY; PRT; 1031 AA.  
 ID 000939 AC 000939;  
 DT 01-JUL-1997 (CREATED)  
 DT 01-JUL-1997 (CREATED)  
 DT 01-JUL-1997 (CREATED)  
 DT 01-JAN-1998 (LAST SEQUENCE UPDATE)  
 DE TELOMERASE REVERSE TRANSCRIPTASE 1.  
 OS EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 OC SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H;  
 RA NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,  
 RA LINGER J.J., HARLEY C.B., CECH T.R.;  
 RL SCIENCE 277: 955-959(1997).  
 DR EMBL; AF015783; G2340169;  
 KW RNA-DIRECTED DNA POLYMERASE,  
 SQ SEQUENCE 989 AA; 116456 MW; FDE74202 CRC32;

SEQUENCE FROM N.A. MEDLINE: 97274210.							
RA. LINGER J., HUGHES T. R., SHEVCHENKO A., MANN M., LUNDBLAAD V., SCIENCE 276:561-567(1997).	RA. CECI T.R., DR. U5964; G2072336; SEQUENCE 1031 AA;	FT SQ	NON-TER SEQUENCE	67 67 AA;	67 8368 MW;	E2A06F2B CRC32;	
Query Match 5.2%; Score 439; DB 3; Length 1031; Best Local Similarity 23.0%; Pred. No. 3.85e-60; Indels 47; Gaps 34; Matches 142; Conservative 168; Mismatches 267; Delns 0; Gaps 0;	Db Qy	Db Qy	Query Match 5.0%; Score 424; Pred. No. 4.19e-57; Best Local Similarity 76.1%; Matches 51; Conservative 10; Mismatches 6; Delns 0; Gaps 0;				
361 FINEFFYNILPDPDFLTGR-NRNFQKVKVYELNKE-LIRKNLLEKINREISMQV 418 464 FVACRLRVLPGLWGSRHNEERFLNTKFK-SLGHAKLSQELT-KMSVTRDCANLRR 522	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
419 ETSAKHFYYEDE-NIYVWKLLRWFEDLYSLIRCFYYEQQSYSKTYYRKNIWD 477 523 SPGVGCVPAAEERLRETLAKLHLWMSVYELLRFSEYYETTFFOKNRFLFYRKSVWS 582	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
478 VIMKMSI-ADLIKETLAEVQEKEV-EEMKKSIGFAPSKLRLPKKTFRPPI--MTF -N 531 583 KLOSIGIQRHQLRKYVLRELSEEVROREARALLTSRLREFPKDGLRPTVMDYVGA 642	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
532 KIVNSDRKTTRKTTNPKLNSLMLKTKRNRFKDPPGFAYVNYDDYMKYBBFVCK-WK 590 643 RTFERKRAERTSRTSYKALF-S-VLNVEARR-PGLIGASVIGLDDIHRAWTFVLVRVA 699	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
591 QVGQPKLFFATMDIECYDVSNEYREKLSTFLKTKLSSDFNIMTAOLIKRKNTIVDS 650 700 QDPPEPFVVKDVGTAYDTIQRDLTEVI-LS-TKPO---NTYCV--RRAVV-O-KA 750	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
651 ERKKEMKDYFRQKFQKALEGQYOPTFSVLENEQNDLNAAKTTLYEAKORNQYFKDNLL 710 751 AHGHYRKA-FRSHVSTLT-DIQPYRMQF-V-PMHQETSPRLDAVTEQSSSLNEASSGLF 806	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
711 QPVIN-ICQVNINFNSKFYKTFQKGIPFGLCVSISSFFYATLLEBSLGFIRDSEHNP 769 807 DVELRMCHHA-VRIGKSYQOCQIPGQSTISLLCSLCYDMENK-L-F---AGIRR 860	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
770 NPNVNLNMRLLTDYLLITTOQNNAVFLIEKLINVSRENGFKNMKQLQTSPLSPSKFAK 829 861 G---LLRLRVDLFLVTPHTLTHAKFLRLTVGVPYGCVVNLRKTVNNFVDEALG- 915	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
830 YGMDSVEQONIYQDYCDWIGISDMKTLALMPNIN-LRIEGLCTLNLMQTKASKWLK 888 916 -GTAFYQMPAHGL-F-FWCGLGLDTTRILEYODSYSSARTSTRASLTFN-RGFKAGRMR 971	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
889 KKLLKSPFL-MNNITHYFRKTITTEDFANKTLNLKLFISGCKYKNCAKE--YKHFKKNLAM 945 972 RKLFGVLRKCHSISLDFLDQVNSLSQTVCNTNIYKILLQAYRFACVQLQPFFHQVWKNPTF 1031	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
946 SSMIDLEVSKTYSVTRA 963 QY 1032 FLRVISDTASLCOYSLKA 1049	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
RESULT 6 O35432 PRELIMINARY; O35432 AC DT 01-JAN-1998 (TREMBLREL. 05, CREATED) O35432 AC DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
O35432 AC DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
TELOMERASE CATALYTIC SUBUNIT (FRAGMENT). MUS MUSCULUS (MOUSE). EUKARYOTA; METAJAOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHENIA; RODENTIA.	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
OC [1] SEQUENCE FROM N.A. DRISSI R., CLEVELAND J.L.; SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL: AF029235; G2605903; -	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy	Db Qy
NON-TER	FT	SQ	FT	SQ	FT	SQ	FT

Db	559 VRSQY-FENTNT G-VLKLENV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVYN---VV-	608	RA STEIBL H.D., SIDDAYATTAM D.; SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
Qy	741 VR-RYAVVQKAHRGHVRAFKSVSTUDLQPMPMRQVVAHLQTSPLRDAYVEQQSSLN	799	RN [3] SEQUENCE FROM N.A.
Db	609 E---M-EIF-K-T - ALWDEKCYIREDGLEQGSSISAPIVDLYKDDLEYSEEFKAS	658	RA STEIBL H.D., SIDDAYATTAM D., KLINGMUELLER W.; PLASMID 34:223-228(1995).
Qy	800 EASGLDDEFLRMCHAVRIRKSYSVQCGQFPGTSLTSLCIGDM-E-NKLF-AG	856	RN [4] SEQUENCE FROM N.A.
Db	659 PSQDTLKLAKLDDDFLTDQOQVINTKLMGCFQKYNARAK-NDKILAVSQSSDDTV	717	RA STEIBL H.D.; THESES ('995); UNIVERSITAET BAYREUTH.
Qy	857 IRRDGLLRLVDDFLVPHLTHAKTFLRTLVGVPEYGVVNLRTKVNNFPVDEALGG	916	DR EMBL; X78052; G459248; -.
Db	718 IQFCAM 723		DR EMBL; X81893; E258949; -.
Qy	917 TAFVQM 922		SQ SEQUENCE 276 AA; 31718 MW; OB54A420 CRC32;
RESULT	8		Query Match 1.7%; Score 141; Pred. No. 4.83e-05; Length 276;
ID	000600 PRELIMINARY; PRT; 234 AA.	Best Local Similarity 33.7%; Matches 30; Conservative 23; Mismatches 30; Indels 6; Gaps 6;	
RP	000600;		
Qy	01-JUL-1997 (TREMBLREL. 04, CREATED)		
Db	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)		
DT	01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)		
FT	PARTID 'O' PROTEIN (FRAGMENT).		
DE	PRB4.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
Qy	SEQUENCE FROM N.A.		
Db	96108975; AMBERGER E., FISHER S., PRAKOPPHOL A., NIECE R.L.; ALEN E.A., AMBERGER E., FISHER S., PRAKOPPHOL A., NIECE R.L.; AM. J. HUM. GENET. 58:143-153 (1996).		
RA	EMBL; S80916; G1911492; -.		
DR	NON_TER 1		
FT	SEQUENCE 234 AA; 23656 MW; B5920075 CRC32;		
SQ			
RESULT	10	Query Match 1.7%; Score 142; DB 2; Length 234; Best Local Similarity 28.2%; Pred. No. 3.44e-05; Matches 40; Conservative 41; Mismatches 52; Indels 9; Gaps 9;	
ID	Q69118 PRELIMINARY; PRT; 296 AA.	Best Local Similarity 38.6%; Matches 39; Conservative 39; Mismatches 33; Indels 9; Gaps 8;	
AC	Q69118; 01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
FT	HYPOTHETICAL PROTEIN (FRAGMENT).		
DE	HUMAN HERPESVIRUS TYPE 4.		
OS	VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;		
OC	GAMMAHERPESVIRINAE.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE: 87284169.		
PFITZNER A.J., TSAI E.C., STROMINGER J.L., SPECK S.H.; RL J. VIROL. 61:2902-2909; 1987.			
DR	EMBL; M17294; G807646; -.		
KW	HYPOTHETICAL PROTEIN.		
FT	NON_TER 1		
SQ	SEQUENCE 296 AA; 31393 MW; D17CEF6F CRC32;		
RESULT	11	Query Match 1.7%; Score 147; DB 11; Length 296; Best Local Similarity 38.6%; Pred. No. 6.21e-06; Matches 20; Conservative 20; Mismatches 33; Indels 9; Gaps 8;	
ID	Q69118 PRELIMINARY; PRT; 574 AA.		
AC	Q69118; 01-JAN-1998 (TREMBLREL. 05, CREATED)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)		
FT	ACTIN ASSOCIATED PROTEIN.		
DE	SPAA4F10.15C.		
OS	UNKNOWN.		
OC	UNCLASSIFIED.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	CONNOR R., CHURCHER C.M.; CONNOR R., CHURCHER C.M.;		
Qy	228 ASRSLPLPKRPRGAPEPER-TPVGQGSWAHPGTRGSD	267	
Db	145 HPKGPEPPQPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPOGGNQSG-P-PP 144		
Qy	177 QLQAAQARPPHASPQRRLGGDRAHNHSVRAHGTRGSPDR-GFCVYSPARPAE-BATSLEGALSCTR 294		
Db	205 APPAGKPGQGPPPQGGRPRP 226		
Qy	295 SHPSVGROHAGGPSTSRPRP 316		
RESULT	9	Query Match 1.7%; Score 148; DB 12; Length 276; Best Local Similarity 28.2%; Pred. No. 3.44e-05; Matches 40; Conservative 41; Mismatches 52; Indels 9; Gaps 9;	
ID	Q46612 PRELIMINARY; PRT; 276 AA.	Best Local Similarity 38.6%; Matches 39; Conservative 39; Mismatches 33; Indels 9; Gaps 8;	
AC	Q46612; 01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
FT	ENTEROBACTER AGGLOMERANS.		
DE	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;		
OS	ENTEROBACTERIAE.		
Qy	IS 1222 GENE ORF-A AND ORF-B.		
Db	[1]		
Qy	SEQUENCE FROM N.A.		
Db	STRAIN-KLEEBERG, 1983;		
RA	LINEAGE: 95255664.		
Qy	STEIBL H.D., LEWECKE F.M.; LEWECKE F.M.;		
Db	LINEAGE: 156:37-4(1995).		
Qy	[2]		
Db	SEQUENCE FROM N.A.		
RA	CONNOR R., CHURCHER C.M.; CONNOR R., CHURCHER C.M.;		

SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.	
RL [2]	SEQUENCE FROM N.A.
RP	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN	EUTHERIA; RODENTIA.
RN	SEQUENCE FROM N.A.
RC	STRAIN=CD-1; TISSUE=LIVER;
RD	MEDLINE; 88273214.
DR	ANN D.K., SMITH M.K., CARLSON D.M.;
SQ	J. BIOL. CHEM. 263:10887-10893(1988).
DR	EMBL; M23236; G567232; -.
Query Match	1.7%; Score 143; DB 13; Length 574;
Best Local Similarity	28.8%; Pred. No. 2.45e-05;
Matches	42; Mismatches 53; Indels 10; Gaps 7;
Db 305	AANIKKRPPPPP-PSRR --NRG-KPPIGNSSNSSLPPPPRPSNAAG-SIPLPPQGR 358
Db 180	ANTQARPPPHASPRRLUCERAWNHSYREAGVPLGLPAPARRGGASAISRSLPKRPR 239
Qy 240	RGAPEPRTYQGSWAHP-GTRGPSPDRGFCVSPARAEATSLEGALSCTRHSHPS 298
Db 417	VPTPPP-SLPPSAPPSSLPPSAPPULPM 441
Qy 299	VGRQHHAGPPS1SRPPREWDTPCPV 324
RESULT 12	PRELIMINARY; PRT; 316 AA.
ID Q99076	AC APPAIPGRSAPALPPLGNARSSTNPP-APPAPPGRSAPALPPLGNARSSTNPP 416
DT 01-NOV-1996	(TREMELREL. 01, CREATED)
DT 01-NOV-1996	(TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998	(TREMELREL. 05, LAST ANNOTATION UPDATE)
DE HOMEOBOX PROTEIN (FRAGMENT)	
GN H99.	
OS HOMO SAPIENS (HUMAN).	
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC EUTHERIA; PRIMATES.	
RN [1]	SEQUENCE FROM N.A.
RP TISSUE=TONSIL;	
RC	NON-BINDING; NUCLEAR PROTEIN; HOMEOBOX; PHOSPHORYLATION.
RX MEDLINE: 91305125.	
RA DEGUCHI Y., KEHRL J.H.;	
RA NUCLEIC ACIDS RES:19:3742-3742(1991);	
CC -1- SIMILARITY: STRONG WITH OTHER "ANTP-TYPE" HOMEOBOX PROTEINS.	
DR EMBL: X56537; E30556; ALT_SEQ.	
DR PIR: S16681; S16681.	
RX DNA-BINDING; NUCLEAR PROTEIN; HOMEOBOX; PHOSPHORYLATION.	
RA NON_TER 1 1	
RA DNA_BIND 70 129	
RA DNA_BIND 112 121	
RA DNA_BIND 15311E76 CRC32;	
SEQUENCE 316 AA; 34713 MW;	
Query Match	1.6%; Score 136; DB 2; Length 316;
Best Local Similarity	30.9%; Pred. No. 2.58e-04;
Matches	20; Mismatches 24; Indels 3; Gaps 3;
Db 202	RWPAASSDCSVGRTGIAPRGPAT-SPRSPRSRPARSAPGAAASPQGPWTH 260
Qy 201	RAWNHSTREAGV-PLGLPAPGARRGGASAISRSLPLPKRPRRG-AAAPEERTPVQGSWAH 258
Db 261	PAPRREQA 268
Qy 259	PGTRGPSP 266
RESULT 13	PRELIMINARY; PRT; 317 AA.
ID Q62103	AC APP-1997 (TREMELREL. 01, CREATED)
DT 01-NOV-1996	(TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998	(TREMELREL. 05, LAST ANNOTATION UPDATE)
DE PROLINE RICH PROTEIN PRECURSOR.	
GN MUS MUSCULUS (MOUSE).	
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC EUTHERIA; RODENTIA.	
RN	SEQUENCE FROM N.A.
RC	STRAIN=CD-1; TISSUE=LIVER;
RD	MEDLINE; 88273214.
DR	ANN D.K., SMITH M.K., CARLSON D.M.;
SQ	J. BIOL. CHEM. 263:10887-10893(1988).
DR	EMBL; M23236; G567232; -.
Query Match	1.6%; Score 133; DB 3; Length 539;
Best Local Similarity	31.7%; Pred. No. 6.92e-04;

Matches 45; Conservative 31; Mismatches 54; Indels 12; Gaps 11;

**Db** 315 AGSPPPPPRGSPTGSLPPPQA-GGSPPPAGT--GSPPPPRQKAPERSPP-TGSP 370  
**Qy** 179 GATQARPPPHASPPRRLGCEAWNHSVREAGVPLGLPAPGARRGSEASRSLPLPKRP 238

**Db** 371 PTGSPP-TGRPPPGPKGSSEESSESSESGPGRGGPRGGPKSSSESSSESEPRGPR 429  
**Qy** 239 RRGAAPEERTP-VGQG-SWAHGRTR-GP-SD-RGFCVVSPARPAAEATSLLEGALSGTR 293

**Db** 430 RSPP-GSPP-TGSPTGRRPR 449  
**Qy** 294 HSPSVGRQHHAGCPPSTSRRPR 315

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RESULT 15 PRELIMINARY; PRT: 585 AA.

ID 041935; 041935;  
AC DT 01-JAN-1998 (TREMELREL. 05, CREATED)  
DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)

CN HYPOTHETICAL 60.2 KD PROTEIN.  
GAMMAY M6.

OS MORINE HERPESVIRUS 68.

OC DSrna VIRUSES, NO RNA STAGE; HERPESVIRIDAE; GAMMAHERPESVIRNAE.

[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=NUMS;  
RC MEDLINE: 97366649  
RA VIRGIN H.W. IV, LATREILLE P., WANSLEY P., HALLSWORTH K., WECK K.E.,  
RA DAL CANTO A.J., SPECK S.H.;  
RL J. VIROL. 71:5894-5904(1997).  
RN [2]  
RP STRAIN=NUMS;  
RC LATREILLE P., WANSLEY P., WATERSTON R.H.;  
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.  
DR EMBL: U97553; G2317934; -.  
KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 585 AA; 60160 MW; B35C72B5 CRC32;

Query Match 1.6%	Score 135	DB 11;	Length 585;
Best Local Similarity 27.6%	Pred. No. 3.59e-04;		
Matches 45; Conservative 37; Mismatches 68; Indels 13; Gaps 11;			

**Db** 342 PPE-ELGGSPTPSAAGRPLDPLPSGPDPRPPLSPGSPTPAPSAG 400  
**Qy** 173 PPLYOLGATAQAPPHASGPRR-L-CERAVNNHSVREA-GVP-LGLPAPGRRGGSA 228

**Db** 401 ARTDLPLGPLPSNGPDPRPPLSPG-GSPP-SPASRAGARIPRSRPPLGP-G 456  
**Qy** 229 SRSLPLPKR-PRTGAAPPERTVGQGSAWHPRTRGSPDGRGCVSPARPAEATSLLEG 287

**Db** 457 SPFRPRPRPRP-PELGGSPTDGPPLPSWG-DDPPTPAPSR 496  
**Qy** 288 ALSGTRASHPSVGRQHHAGPPSTSRRPRPWDTCPVVAETKH 330

Search completed: Thu Jul 30 14:51:34 1998  
Job time : 147 secs.